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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/834,760

DATE: 10/12/2001

TIME: 12:10:57

Input Set : A:\19874410.app

Output Set: N:\CRF3\10122001\I834760.raw

3 <110> APPLICANT: Austin, Richard C  
 4 Chan, Anthony K.C.  
 5 Berry, Leslie  
 6 Hamilton Civic Hospitals Research Development Inc.  
 8 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING THROMBIN  
 9 GENERATION AT THE SURFACE OF CELLS  
 11 <130> FILE REFERENCE: 019874-000410US  
 13 <140> CURRENT APPLICATION NUMBER: US 09/834,760  
 14 <141> CURRENT FILING DATE: 2001-04-12  
 16 <150> PRIOR APPLICATION NUMBER: US 60/197,146  
 17 <151> PRIOR FILING DATE: 2000-04-14  
 19 <160> NUMBER OF SEQ ID NOS: 5  
 21 <170> SOFTWARE: PatentIn Ver. 2.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 24  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Artificial Sequence  
 28 <220> FEATURE:  
 29 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer AB10230  
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 62 <213> ORGANISM: Homo sapiens  
 64 <220> FEATURE:  
 65 <223> OTHER INFORMATION: GRP78/BiP amino acid sequence  
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 69 1 5 10 15  
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72	20	25	30	
74	Ile Asp Leu Gly Thr Thr Tyr Ser Cys Val Gly Val Phe Lys Asn Gly			
75	35	40	45	
77	Arg Val Glu Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Thr Pro Ser			
78	50	55	60	
80	Tyr Val Ala Phe Thr Pro Glu Gly Glu Arg Leu Ile Gly Asp Ala Ala			
81	65	70	75	80
83	Lys Asn Gln Leu Thr Ser Asn Pro Glu Asn Thr Val Phe Asp Ala Lys			
84	85	90	95	
86	Arg Leu Ile Gly Arg Thr Trp Asn Asp Pro Ser Val Gln Gln Asp Ile			
87	100	105	110	
89	Lys Phe Leu Pro Phe Lys Val Val Glu Lys Lys Thr Lys Pro Tyr Ile			
90	115	120	125	
92	Gln Val Asp Ile Gly Gly Gln Thr Lys Thr Phe Ala Pro Glu Glu			
93	130	135	140	
95	Ile Ser Ala Met Val Leu Thr Lys Met Lys Glu Thr Ala Glu Ala Tyr			
96	145	150	155	160
98	Leu Gly Lys Lys Val Thr His Ala Val Val Thr Val Pro Ala Tyr Phe			
99	165	170	175	
101	Asn Asp Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Gly			
102	180	185	190	
104	Leu Asn Val Met Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala			
105	195	200	205	
107	Tyr Gly Leu Asp Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp			
108	210	215	220	
110	Leu Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly			
111	225	230	235	240
113	Val Phe Glu Val Val Ala Thr Asn Gly Asp Thr His Leu Gly Gly Glu			
114	245	250	255	
116	Asp Phe Asp Gln Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys			
117	260	265	270	
119	Lys Thr Gly Lys Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu			
120	275	280	285	
122	Arg Arg Glu Val Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln			
123	290	295	300	
125	Ala Arg Ile Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu			
126	305	310	315	320
128	Thr Leu Thr Arg Ala Lys Phe Glu Glu Leu Asn Met Asp Leu Phe Arg			
129	325	330	335	
131	Ser Thr Met Lys Pro Val Gln Lys Val Leu Glu Asp Ser Asp Leu Lys			
132	340	345	350	
134	Lys Ser Asp Ile Asp Glu Ile Val Leu Val Gly Gly Ser Thr Arg Ile			
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137	Pro Lys Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu Pro			
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140	Ser Arg Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr Gly Ala Ala Val			
141	385	390	395	400
143	Gln Ala Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val Leu			
144	405	410	415	

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146 Leu Asp Val Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly Val  
147 420 425 430  
149 Met Thr Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys Ser  
150 435 440 445  
152 Gln Ile Phe Ser Thr Ala Ser Asp Asn Gln Pro Thr Val Thr Ile Lys  
153 450 455 460  
155 Val Tyr Glu Gly Glu Arg Pro Leu Thr Lys Asp Asn His Leu Leu Gly  
156 465 470 475 480  
158 Thr Phe Asp Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln  
159 485 490 495  
161 Ile Glu Val Thr Phe Glu Ile Asp Val Asn Gly Ile Leu Arg Val Thr  
162 500 505 510  
164 Ala Glu Asp Lys Gly Thr Gly Asn Lys Asn Lys Ile Thr Ile Thr Asn  
165 515 520 525  
167 Asp Gln Asn Arg Leu Thr Pro Glu Glu Ile Glu Arg Met Val Asn Asp  
168 530 535 540  
170 Ala Glu Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Arg Ile Asp  
171 545 550 555 560  
173 Thr Arg Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile  
174 565 570 575  
176 Gly Asp Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu  
177 580 585 590  
179 Thr Met Glu Lys Ala Val Glu Glu Lys Ile Glu Trp Leu Glu Ser His  
180 595 600 605  
182 Gln Asp Ala Asp Ile Glu Asp Phe Lys Ala Lys Lys Lys Glu Leu Glu  
183 610 615 620  
185 Glu Ile Val Gln Pro Ile Ile Ser Lys Leu Tyr Gly Ser Ala Gly Pro  
186 625 630 635 640  
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189 645 650  
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193 <211> LENGTH: 2007  
194 <212> TYPE: DNA  
195 <213> ORGANISM: Homo sapiens  
197 <220> FEATURE:  
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202 gccccccgag gaggaggaca agaaggagga cgtggccacg gtggtcggca tcgacacctggg 120  
203 gaccacctac tcctgcgtcg gcgtgttcaa gaacggccgc gtggagatca tcgccaacga 180  
204 tcagggcaac cgcacacgc cgtcctatgt cgccttact cctgaaggaaa aacgtctgat 240  
205 tggcgatgcc gccaagaacc agctcacctc caaccccgag aacacggctt ttgacgccaa 300  
206 gccgcgtcattt ggccgcacgt ggaatgaccc gtctgtcag caggacatca agttcttgcc 360  
207 gttcaagggtt gttaaaaaaa aactaaacc atacattcaa gttgatattt gaggtggca 420  
208 aacaaaagaca tttgctcctg aagaaatttc tgccatggtt ctcactaaaa tgaaagaaa 480  
209 cgctgaggct tatttggaa agaaggttac ccatgcgtt gttactgtac cagcctattt 540  
210 taatgatgcc caacccaaag caacccaaaga cgctggaact attgctggcc taaatgttat 600  
211 gaggatcattt aacgagccta cggcagctgc tattgcttat ggcctggata agagggaggg 660  
212 ggagaagaac atcctggtgt ttgacctggc tggcgttacc ttcttctcac 720

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213 cattgacaat ggtgtcttcg aagttgtggc cactaatggc gatactcatc tgggtggaga 780  
214 agactttgac cagcgtgtca tggAACACTT catcaaactg tacaaaaaga agacgggcaa 840  
215 agatgtcagg aaagacaata gagctgtgca gaaactccgg cgcgaggtag aaaaggccaa 900  
216 acgggcccctg tcttcgtcgc atcaagcaag aattgaaatt gagtccttct atgaaggaga 960  
217 agacttttct gagaccctga ctcgggccaa atttgaagag ctcaacatgg atctgttccg 1020  
218 gtctactatg aagcccggtcc agaaaagtgtt ggaagattct gatttgaaga agtctgatat 1080  
219 tggatggaaatt gttctgttg gtggctcgac tcgaattcca aagattcagc aactggtaa 1140  
220 agagttcttc aatggcaagg aaccatcccg tggcataaac ccagatgaag ctgttagcgta 1200  
221 tggtgctgct gtccaggctg gtgtgctctc tggtgatcaa gatacagggtg acctggtaact 1260  
222 gcttgatgta tggccccccta cacttggat tggaaactgtg ggaggtgtca tgaccaaact 1320  
223 gattccaagg aacacagtgg tgccttaccaa gaagtctcag atctttctta cagcttctga 1380  
224 taatcaacca actgttacaa tcaaggctta tgaaggtgaa agacccctga caaaagacaa 1440  
225 tcatcttctg ggtacatttg atctgactgg aattcctctt gctcctcgta gggtcccaca 1500  
226 gattgaagtc acctttgaga tagatgtgaa tggatttctt cgagtgacag ctgaagacaa 1560  
227 gggtaacagg aacaaaata agatcacaat caccaatgac cagaatcgcc tgacacactga 1620  
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**VERIFICATION SUMMARY**

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